

FIG. 1

1 MNDPNS CVDNATV CSGA SC - - - VVPESNFNNI LSV LSTV ISBT
 1 MRA - - NC - SSSSAC PAN SSEEELPVGLEVHGN LELV FTVV TCH230

38 L T I L L A L V M F S M G C N V E I K K F L G H I K R P W G I C V G F L C Q F G ISBT
 38 S T V M M G L L M F S L G C S V E I R K L W S H I R R P W G I A V G L L C Q F G TCH230

78 I M P L T G F I L S V A F D I L P L Q A V V V L I I G C C P G G T A S N I L A Y ISBT
 78 L M P F T A Y L L A I S F S L K P V Q A I A V L I M G C C P G G T I S N I F T F TCH230

118 W V D G D M D L S V S M T T C S T L L A L G M M P L C L L I Y T K M W V D S G S ISBT
 118 W V D G D M D L S I S M T T C S T V A A L G M M P L C I Y L Y T W S W S L Q Q N TCH230

158 I V I P Y D N I G T S L V A L V V P V S I G M F V N H K W P Q K A K I I L K I G ISBT
 158 L T I P Y Q N I G I T L V C L T I P V A P G V Y V N Y R W P K Q S K I I L K I G TCH230

198 S I A G A I L I V L I A V V G G I L Y Q S A W I I A P K L W I I G T I F P V A G ISBT
 198 A V V G G V L L L V V A V A G V V L A K G S W N S D I T L L T I S F I F P L I G TCH230

238 Y S L G P L L A R I A G L P W Y R C R T V A F E T G M Q N T Q L C S T I V Q L S ISBT
 238 H V T G P L L A L P T H Q S W Q R C R T I S L E T G A Q N I Q M C I T M L Q L S TCH230

278 F T P E E L N V V F T F P L I Y S I F Q L A F A A I F L G F Y V A Y K K C - - - ISBT
 278 F T A E E L V Q M L S F P L A Y G L F Q L I D G P L I V A A Y Q T Y K R R L K N TCH230

315 - H G K N K A - - - E I P E S K E N G T E P E S S F Y - - - K A N G G P Q P D E ISBT
 318 K H G K K N S G C T E V C H T R K S T S S R E T N A F L E V N E E G A I T P G P TCH230

348 - - - - - K ISBT
 358 P G P M D C H R A L E P V G H I T S C E TCH230

FIG. 2

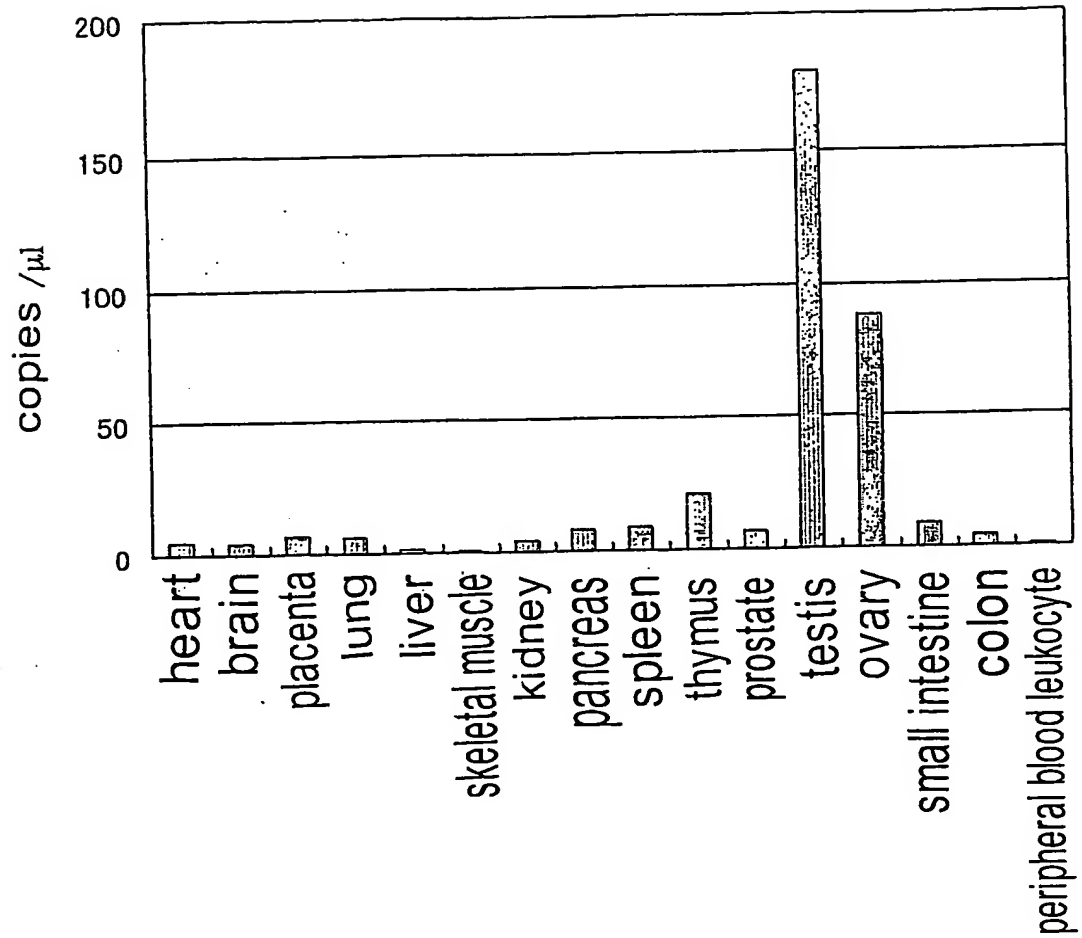


FIG. 3

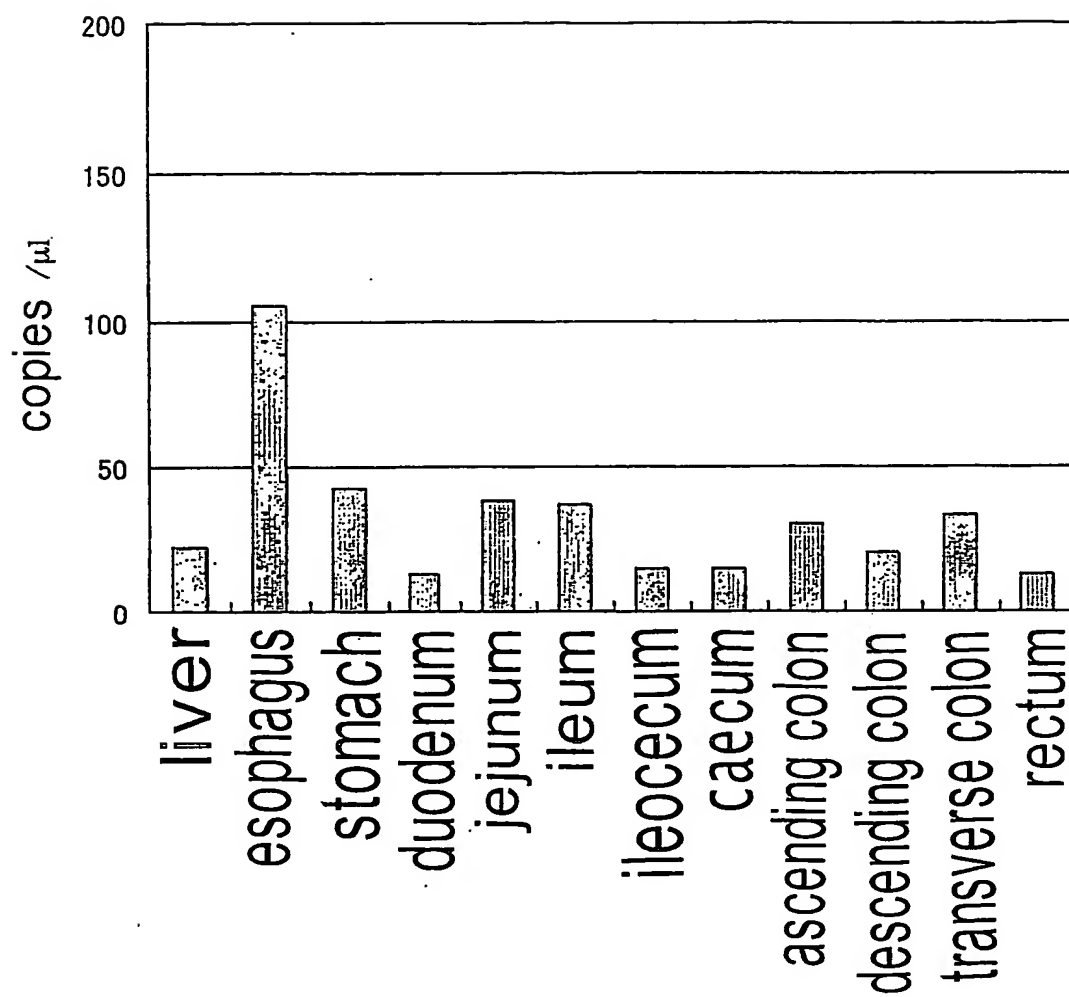


FIG. 4

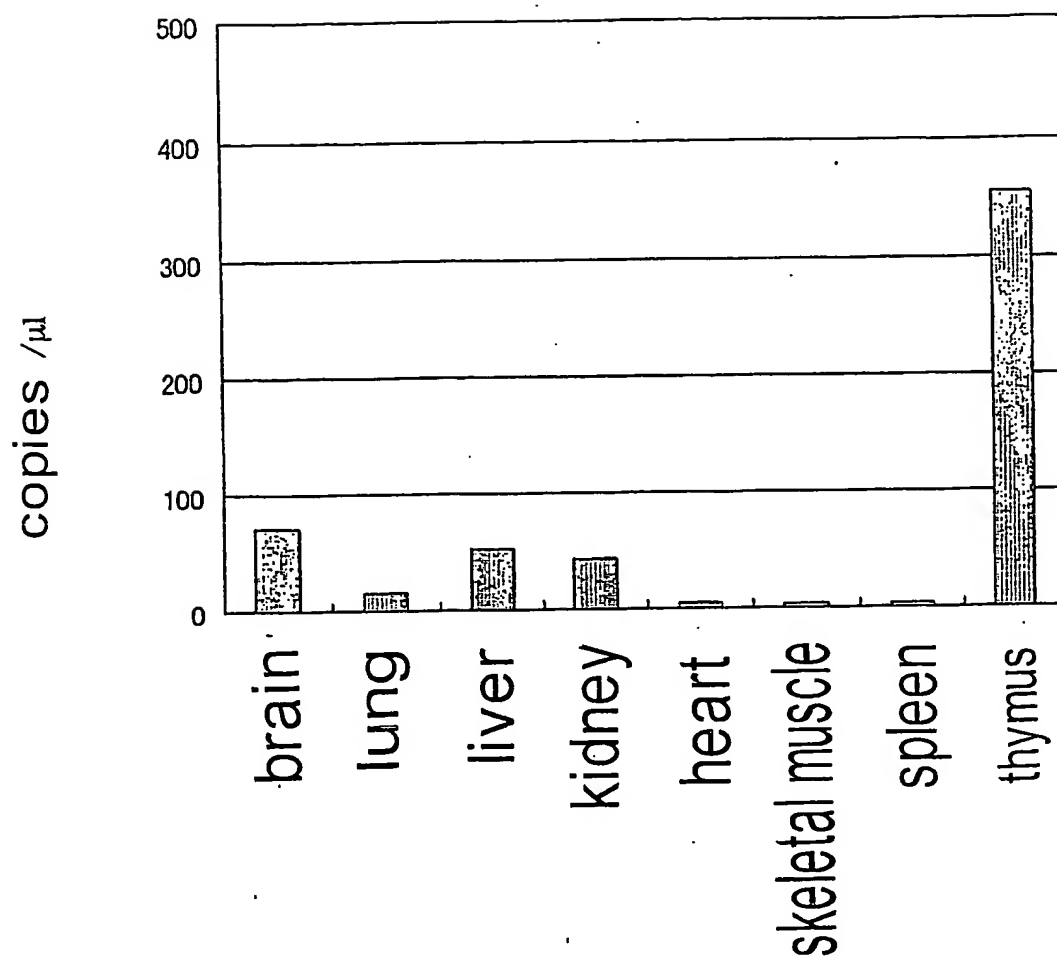


FIG. 5

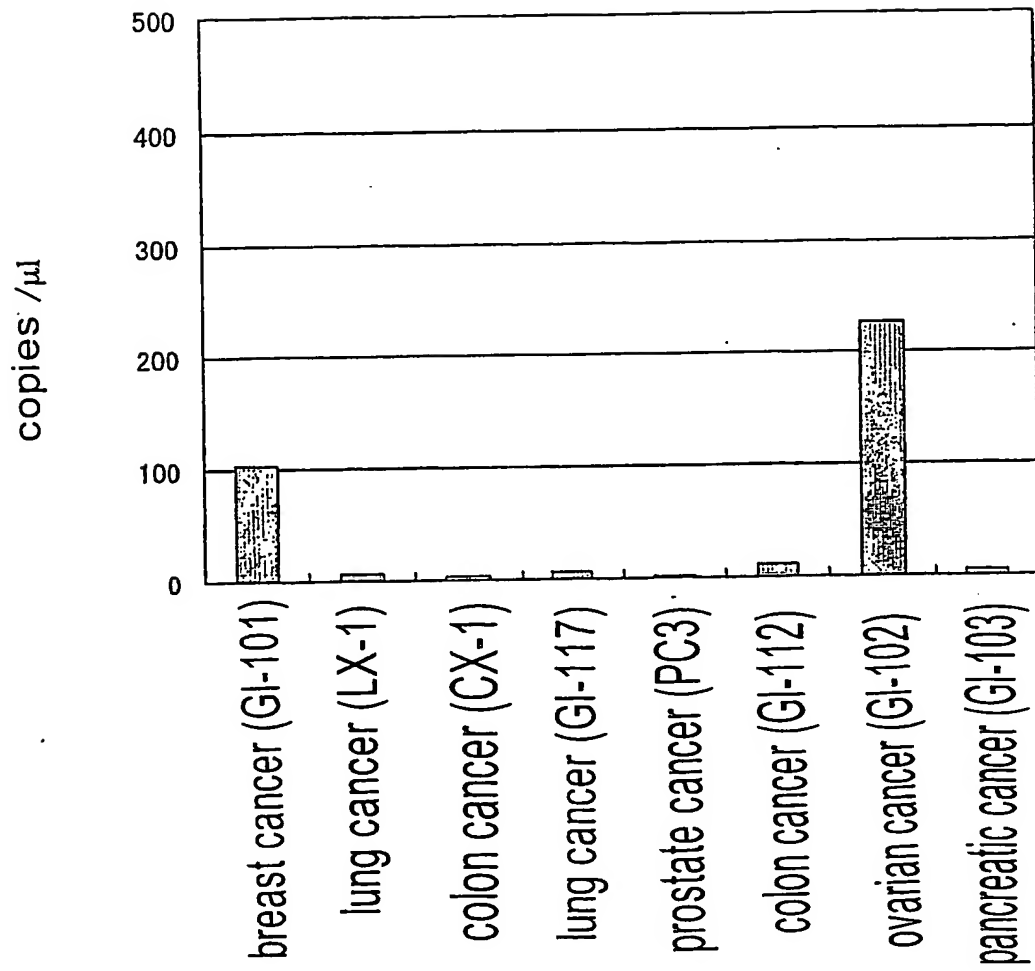


FIG. 6

		TM1		
TCH234	MAIQMFVYSPNCT-----LLIVAESEASSDLNESANSTAYASNPWFARASSE-----			54
ratNHE4	MGEAMLRAPSSKWT-----LLIMVLTLEASSYVNESSSPGQOTPDARFAASSSD-----			54
humanNHE2	MEH-----LGNRSTRAPLPMLLLQVAGPVGAETLLNAPRAMGTSSSPPEASVVAPGTTLFE			65
		TM2	TM3	
TCH234	EGISVFELDYYVQIPYEVTLWILLASLAKIGFHLHYRLEGLMPESCLLTIVGALVGGIIFGTDHKSPPV			124
ratNHE4	ERISVFELDYYVQIPYEVTLWILLASLAKIGFHLHYRLEGLMPESCLLTIVGALVGGIIFGTDHKSPPV			124
humanNHE2	SRLPVEFLDYPHVQIFETFLWILLASLAKIGFHLHYRLEGLMPESCLLTIVGALVGGIIFGTDHKSPPV			135
		TM4	TM5	
TCH234	MDSSIFLYLLPPIVLEGGYFMPTRPFFENIGSILWVAVLGALINALGIGLSLYLCCQKAFGLGDNLI			194
ratNHE4	MDSSIFLYLLPPIVLEGGYFMPTRPFFENIGSILWVAVLGALINALGIGLSLYLCCQKAFGLGDNLI			194
humanNHE2	MKTDPVFLYLLPPIVLDAGYFMPTRPFFENIGSILWVAVLGALINALGIGLSLYLCCQKAFGLGDNLI			205
		TM6	TM7	
TCH234	QNLLFGSLISAVDPVAVLAVFEEARVNEQLYMMIPGEALLNDGIVTVLYNMLIAFTKMHKFEDIETVDII			264
ratNHE4	QNLLFGSLISAVDPVAVLAVFEEARVNEQLYMMIPGEALLNDGIVTVLYNMLIAFTKMHKFEDIETVDII			264
humanNHE2	QNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGESLLNDAVTVVLYNLPKSECOMK---TETIIVF			272
		TM8	TM9	
TCH234	AGCARFIVVGLGGVLPGLVFGFISAFITRFTQNISAIPLIVFMFSYLSYLAETLYLSGILAITACAVT			334
ratNHE4	AGCARFIVVGLGGVLPGLVFGFISAFITRFTQNISAIPLIVFMFSYLSYLAETLYLSGILAITACAVT			334
humanNHE2	AGINNEFVVGIGGVIGFGLGFIAFTTRFTENIRVIEPIFVFLYSYLSYITAEFHLSGIMAITACAVT			342
		TM10	TM11	
TCH234	MKKYVEENVVSQTSYTTIKYFMKMLSSVSETLIFIPMGVSTVGKNHEWNWAFVCTLAFCQIWRRAISVEAR			404
ratNHE4	MKKYVEENVVSQTSYTTIKYFMKMLSSVSETLIFIPMGVSTVGKNHEWNWAFVCTLAFCQIWRRAISVEAR			404
humanNHE2	MKKYVEENVVSQTSYTTIKYFMKMLSSVSETLIFIPMGVSTVGKNHEWNWAFVCTLAFCQIWRRAISVEAR			412
		TM12	TM13	
TCH234	FYISNQFRFTFFPSIKDCLIFYSYGVGAGSFLAFLLPISLFPKRMFVTATLVVYFTVFIQGITVGP			474
ratNHE4	FYVSNQFRFTFFPSIKDCLIFYSYGVGAGSFLAFLLPISLFPKRMFVTATLVVYFTVFIQGITVGP			474
humanNHE2	TOVINRFRFTFTFKDCLIFYSYGVGAGSFLAFLLPISLFPKRMFVTATLVVYFTVFIQGITVGP			482
TCH234	VRYLDVKKTNKKE-SINEELHIRLMDHLKAGIEDVCGHWSHYQVRDKFKKFDHRYLRKILIRNPKSSI			543
ratNHE4	VRYLDVKKTNKKE-SINEELHIRLMDHLKAGIEDVCGHWSHYQVRDKFKKFDHRYLRKILIRNPKSSI			543
humanNHE2	VEFLDVKRSNKKQAVSEEIYCRIFDVHTGIEDVCGHWSHYQVRDKFKKFDHRYLRKILIRNPKSSI			552
TCH234	VSLEYKLEMKQAIENVETGILSSVSPSIHQAQRIQGIKRLSPEDVESIRDILTSNMYQVRQRTLSYNKY			613
ratNHE4	VSLEYKLEMKQAIEMAETGLSSVSPSIHQAQRIQGIKRLSPEDVESMRDILTRNMYQVRQRTLSYNKY			613
humanNHE2	VSLEYKLEMKQAIEMAETGMISTVPTFASLNDCEKIRKVTSSSETDEIRRELSRNLYQIRQRTLSYNKH			622
TCH234	NLKPQTSEKQAKEILIRRONTLRESMRKQHSPLWPKPAGTKNIRYLSYFYGNPQSG-RDTRANGFSDD			682
ratNHE4	NLKPQTSEKQAKEILIRRONTLRESLRKGOSLPWPKPAGTKNIRYLSYFYGNPQSG-RGARAN---ES			678
humanNHE2	SETADTSERQAKEILIRRRHSLRESIRKDSINREHRNSTSTSYLSLEKNTKLEKLOKRTISIAIGN			692
TCH234	SSDFGSPSIFSAQSRIGSLQKQEQEIIEMKSLERGRKAFSFGYQRNTSQEYFG-----			739
ratNHE4	TGNE-----CWL-----LH-----FT-----			690
humanNHE2	SSDSADAGIT-----VLNLQPR-RRRFLHEQFSKKSQSYKMEWKNEVDVDSGRDMPSTPTPHSREK			756
TCH234	VERRVARRPKPIPHAVDEEGSGGE-SEGKASLVEVRSRRTDHGHSRDHHRSHSPLQKK			798
ratNHE4	-----LCRPM-----VEKINGPG-----GQETQPRLLCRNLN			717
humanNHE2	TQTSGLOQPLLSKDQSGSREDSLTEGIPPKPPPLVRRRSEPCSRKARFGSEK-----P			812

FIG. 7

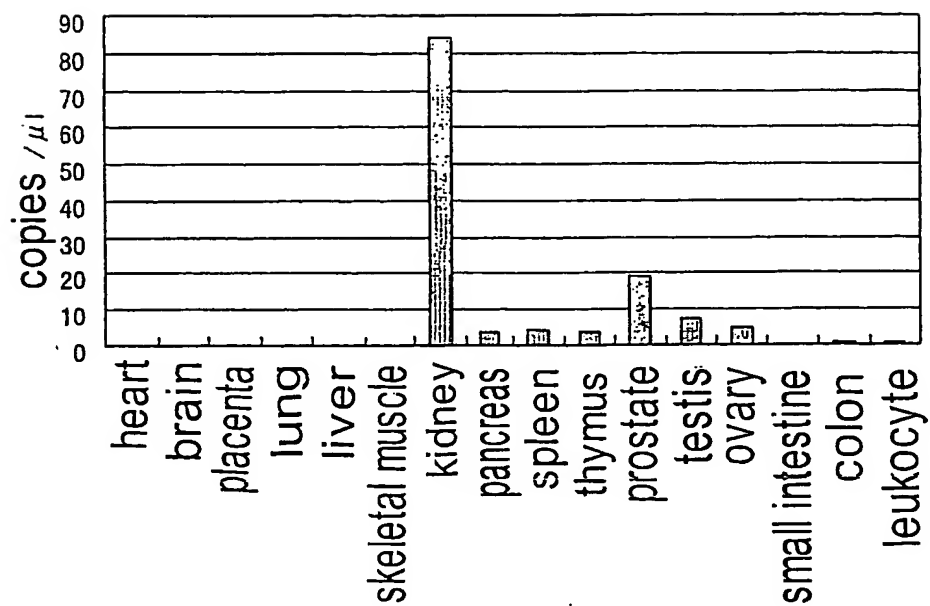


FIG. 8

[illegible]

FIG. 9

400	F	K	K	C	S	I	A	G	V	T	Y	G	H	F	P	E	L	A	R	E	Q	S	S	D	D	F	-	C	-	-	-	-	R	M	T	S	C	T	N	D	S	C	D	F	N	D	P	R	L	L	K	N	I	E	D	Q	H	P	T	A	MATP8A2
421	F	K	K	C	T	I	A	G	V	A	Y	G	H	V	P	E	-	-	-	-	P	E	D	Y	G	C	S	P	D	E	W	Q	N	S	Q	F	G	D	E	K	T	F	S	D	S	S	L	L	E	N	L	Q	N	N	H	P	T	A	ATP8A1		
400	F	K	K	C	S	I	A	G	V	T	Y	G	H	F	P	E	L	A	R	E	P	S	S	D	D	F	-	C	-	-	-	-	-	R	M	P	P	C	S	D	S	C	D	F	D	D	P	R	L	L	K	N	I	E	D	R	H	P	T	A	TCH212
455	P	C	I	Q	E	F	L	T	L	L	A	V	C	H	T	V	V	P	E	K	D	G	D	E	I	I	Y	Q	A	S	S	P	D	E	A	A	L	V	K	G	A	K	K	L	G	F	V	F	T	G	R	T	P	Y	S	V	I	I	E	A	MATP8A2
475	P	I	I	C	E	F	L	T	M	M	A	V	C	H	T	A	V	P	E	R	E	G	D	K	I	I	Y	Q	A	A	S	P	D	E	G	A	L	V	R	A	A	K	Q	L	N	F	V	F	T	G	R	T	P	D	S	V	I	I	D	S	ATP8A1
455	P	C	I	Q	E	F	L	T	L	L	A	V	C	H	T	V	V	P	E	K	D	G	D	N	I	I	Y	Q	A	S	S	P	D	E	A	A	L	V	K	G	A	K	K	L	G	F	V	F	T	A	R	T	P	F	S	V	I	I	E	A	TCH212
515	M	G	Q	E	Q	T	F	G	I	L	N	V	L	E	F	S	S	D	R	K	R	M	S	V	I	V	R	L	P	S	G	Q	L	R	L	Y	C	K	G	A	D	N	V	I	F	E	R	L	S	K	D	S	K	Y	M	E	T	L	C	MATP8A2	
535	L	G	Q	E	R	Y	E	L	L	N	V	L	E	F	S	S	A	R	K	R	M	S	V	I	V	R	T	P	S	G	K	L	R	L	Y	C	K	G	A	D	T	V	I	Y	D	R	L	A	E	T	S	K	Y	K	E	I	T	L	K	ATP8A1	
515	M	G	Q	E	Q	T	F	G	I	L	N	V	L	E	F	S	S	D	R	K	R	M	S	V	I	V	R	T	P	S	G	R	L	R	L	Y	C	K	G	A	D	N	V	I	F	E	R	L	S	K	D	S	K	Y	M	E	T	L	C	TCH212	
575	H	L	E	Y	F	A	T	E	G	L	R	T	L	C	V	A	Y	A	D	L	S	E	N	E	Y	E	E	W	L	K	V	Y	Q	E	A	S	I	I	L	K	D	R	A	Q	R	L	E	E	C	Y	E	I	E	K	N	L	L	L	MATP8A2		
595	H	L	E	Q	F	A	T	E	G	L	R	T	L	C	F	A	V	A	E	I	S	E	S	D	F	Q	E	W	R	A	V	Y	Q	R	A	S	T	S	V	Q	N	R	L	L	K	L	E	E	S	Y	E	L	I	E	K	N	L	Q	L	L	ATP8A1
575	H	L	E	Y	F	A	T	E	G	L	R	T	L	C	V	A	Y	A	D	L	S	E	N	E	Y	E	E	W	L	K	V	Y	Q	E	A	S	T	I	L	K	D	R	A	Q	R	L	E	E	C	Y	E	I	E	K	N	L	L	L	TCH212		
635	G	A	T	A	I	E	D	R	L	Q	A	G	V	P	E	T	I	A	T	L	L	K	A	E	I	K	I	W	V	L	T	G	D	K	Q	E	T	A	I	N	I	G	Y	S	C	R	L	V	S	Q	N	M	A	L	I	L	L	K	E	D	MATP8A2
655	G	A	T	A	I	E	D	K	L	Q	D	Q	V	P	E	T	I	E	T	L	M	K	A	D	I	K	I	W	V	L	T	G	D	K	Q	E	T	A	I	N	I	G	H	S	C	K	L	L	K	K	N	M	G	M	I	V	I	N	E	G	ATP8A1
635	G	A	T	A	I	E	D	R	L	Q	A	G	V	P	E	T	I	A	T	L	L	K	A	E	I	K	I	W	V	L	T	G	D	K	Q	E	T	A	I	N	I	G	Y	S	C	R	L	V	S	Q	N	M	A	L	I	L	L	K	E	D	TCH212
695	S	L	D	A	T	R	A	A	I	T	Q	H	C	T	D	L	G	N	L	L	G	K	E	N	D	V	A	L	I	I	D	G	H	T	L	K	Y	A	L	S	F	E	V	R	R	S	F	L	D	L	A	L	S	C	K	A	V	I	C	MATP8A2	
715	S	L	D	G	T	R	E	T	L	S	R	H	C	T	T	L	G	D	A	L	R	K	E	N	D	F	A	L	I	I	D	G	K	T	L	K	Y	A	L	T	F	G	V	R	Q	Y	F	L	D	L	A	L	S	C	K	A	V	I	C	ATP8A1	
695	S	L	D	A	T	R	A	A	I	T	Q	H	C	T	D	L	G	N	L	L	G	K	E	N	D	V	A	L	I	I	D	G	H	T	L	K	Y	A	L	S	F	E	V	R	R	S	F	L	D	L	A	L	S	C	K	A	V	I	C	TCH212	
755	R	V	S	P	L	Q	K	S	E	I	V	D	V	V	K	K	R	V	K	A	I	T	L	A	I	G	D	G	A	N	D	V	G	M	I	Q	T	A	H	V	G	V	G	I	S	G	N	E	G	M	Q	A	T	N	N	S	D	Y	A	I	MATP8A2
775	R	V	S	P	L	Q	K	S	E	I	V	D	V	V	K	K	R	V	K	A	I	T	L	A	I	G	D	G	A	N	D	V	S	M	I	Q	T	A	H	V	G	V	G	I	S	G	N	E	G	L	Q	A	N	S	S	D	Y	S	I	ATP8A1	
755	R	V	S	P	L	Q	K	S	E	I	V	D	V	V	K	K	R	V	K	A	I	T	L	A	I	G	D	G	A	N	D	V	G	M	I	Q	T	A	H	V	G	V	G	I	S	G	N	E	G	M	Q	A	T	N	N	S	D	Y	A	I	TCH212

FIG. 10

815	AQFSYL	EKLL	LVHGAW	SYNRY	TKCILYCFYKN	VVLYII	ELWF	AFVNGFS	QILFER	WCIG	mATP8A2
835	AQFKYL	KNLL	MHGA	NYNRY	SKCILYCFYKN	IVLYII	ELWF	AFVNGFS	QILFER	WCIG	ATP8A1
815	AQFSYL	EKLL	LVHGAW	SYNRY	TKCILYCFYKN	VVLYII	ELWF	AFVNGFS	QILFER	WCIG	TCH212
TM6											
875	LYNV	IFTAL	PPFT	TLGIF	ERSCT	QESML	RFR	QLYR	ITQN	AEGF	mATP8A2
895	LYNV	MTAM	PPPL	TLGIF	ERSCT	QRKEN	MLKYP	ELYK	TSQN	ALDF	ATP8A1
875	LYNV	IFTAL	PPFT	TLGIF	ERSCT	QESML	RFR	QLYR	ITQN	AEGF	TCH212
TM7											
935	LFWV	PMKAL	EHDT	TPVTS	GHA	TDYLF	VGN	IVY	TYV	TVCL	mATP8A2
955	LFWV	PMKAL	QYGT	AFGNG	KTS	TDYLF	VGN	IVY	TYV	TVCL	ATP8A1
935	LFWV	PMKAL	EHDT	TPVTS	GHA	TDYLF	VGN	IVY	TYV	TVCL	TCH212
TM8											
995	MLI	WLV	FGV	YS	TI	PI	APDM	KQA	TM	VLS	mATP8A2
1015	I	AL	WV	FG	I	YS	SL	WPA	I	PM	ATP8A1
995	MLT	WLV	FG	I	YS	TI	PI	APDM	KQA	TM	TCH212
TM9											
1055	CKKT	LE	EV	QEL	E	TKSR	VMG	KAM	L	RDS	mATP8A2
1075	TA	FK	TL	V	DE	V	QEL	E	AKS	QDP	ATP8A1
1055	CKKT	LE	EV	QEL	E	TKSR	RV	LG	KAV	L	TCH212
TM10											
1115	V	SH	GY	A	F	S	Q	EE	H	G	mATP8A2
1131	L	L	H	G	Y	A	F	S	Q	DE	ATP8A1
1115	V	P	H	G	Y	A	F	S	Q	EE	TCH212

FIG. 11

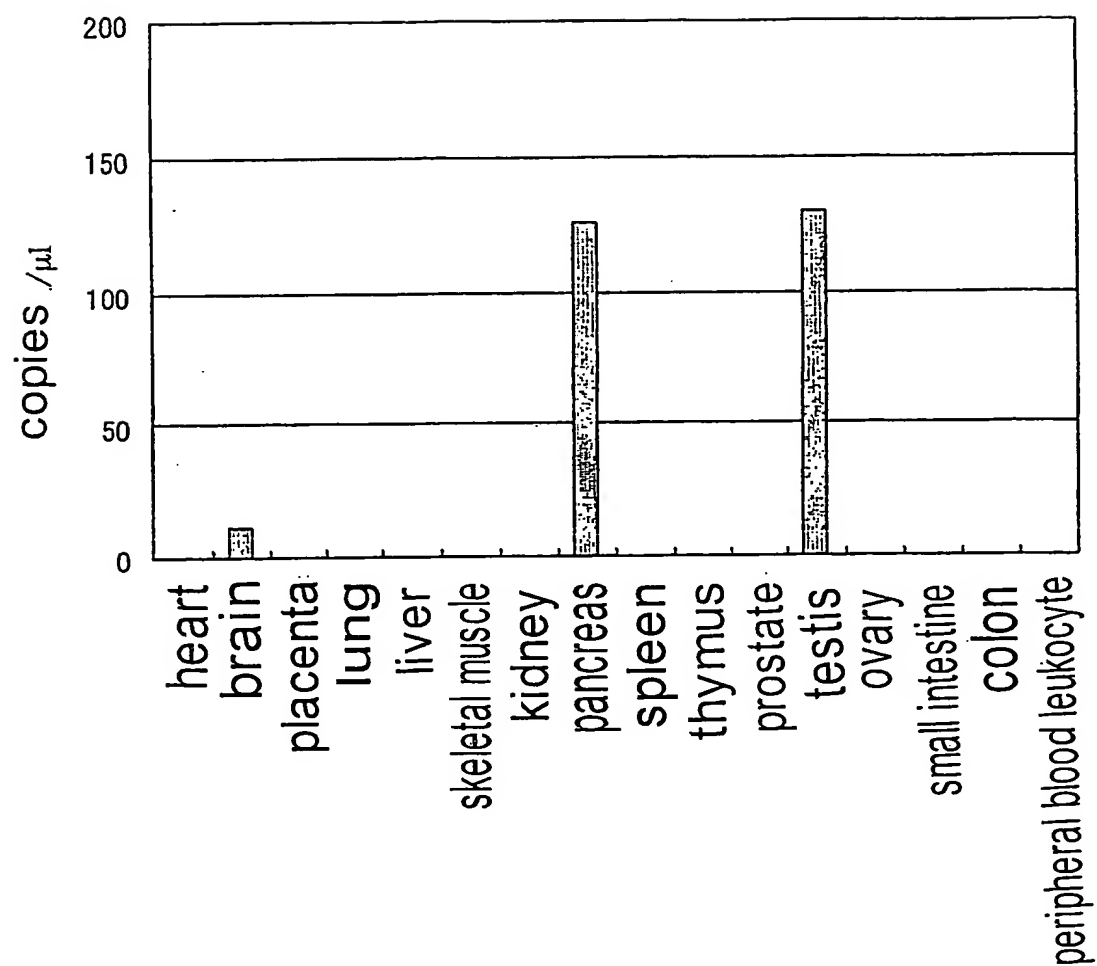


Fig. 12

FIG. 12

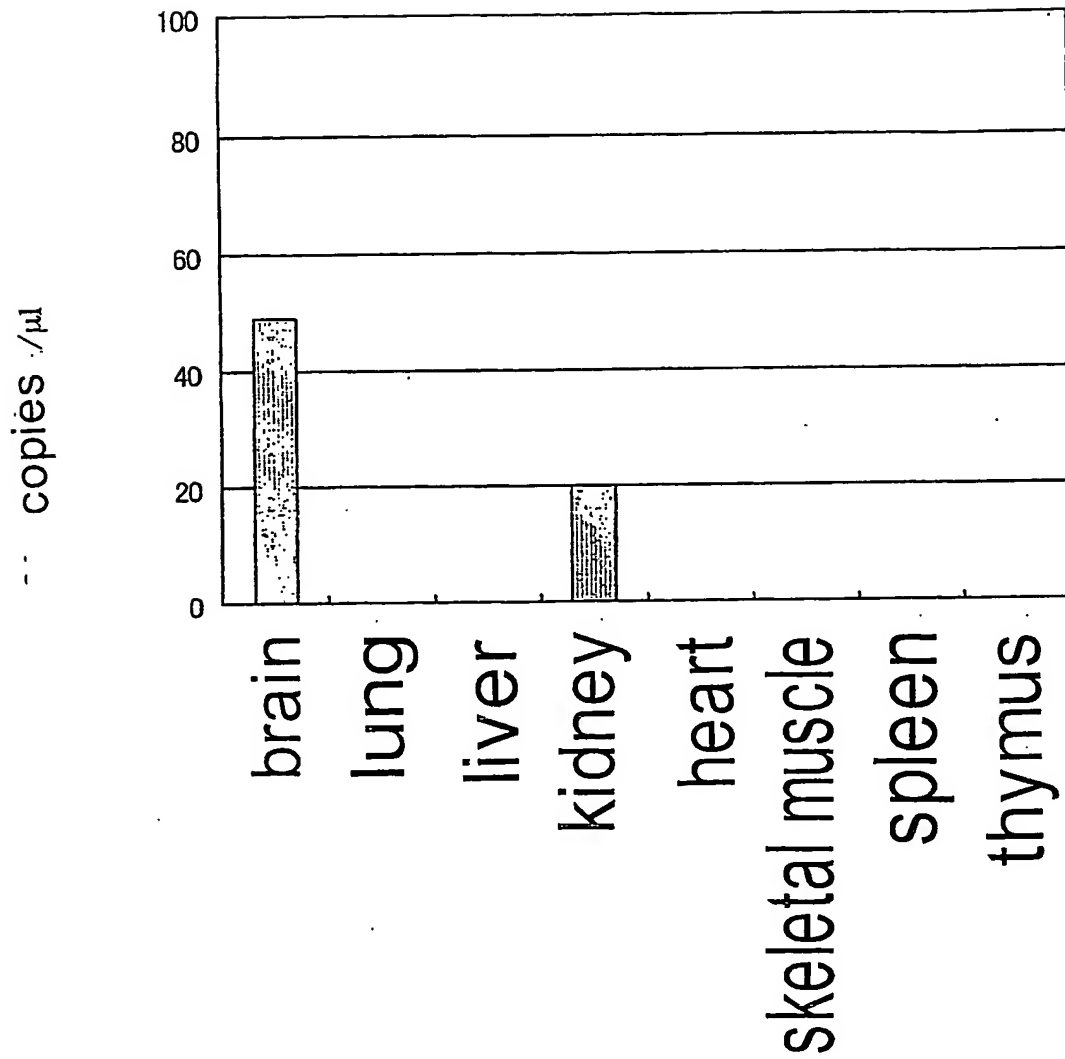


FIG. 13

1 M K X W S S T D L G A A A D P L Q K D T C P D P L D G D P N S R P P P A K P O L S T A K S R T R hVR1
 1 M K A H P K E M V P L N G K R V A A P S - - - - - G N P A V L P E K R P A E I T P T K K S A H TCH200
 49 L F - - - - - G K G D S E E A F P V D C P H E E G E L D S C P T I T V S P V I T I Q R P G hVR1
 43 F F L E I E G F E P N P T V A K T S P P V F S K P M D S N I R Q C I S G N C D D M D S P Q S P Q TCH200
 89 D G P T G A R L L S Q D S V A S T E K T L R L Y D R R - - - S I F E A V A Q N N C Q D L E S L hVR1
 91 D D V T E T P S N P N S P S A Q L A K E E Q R R K K R R L K K R I F A A V S E G C V E E L V E L TCH200
 134 L L F L Q K - - S K K H L T D - - - - - N E F K D P E T G K T C L L K A M L N L H D G Q N T T hVR1
 139 L V E L Q E L C R R R H D E D V P D F L M H K L T A S D T G K T C L M K A L L N I N P N T K E I TCH200
 174 I P L L L E I A R Q T D S L K E L V N A S Y T D S Y Y K G Q T A L H I A I E R R N M A L V T L L hVR1
 187 V R I L L A F A E E N D I L G R F I N A E Y T E E A Y E G Q T A L N I A I E R R Q G D I A A L TCH200
 222 V E N G A D V Q A A A H G D F F K K T K G R P G F Y F G E L P L S L A A C T N Q L G I V K F L L hVR1
 235 I A A G A D V N A H A K G A F P N P K Y Q H E G F Y F G E T P L A L A A C T N Q P E I V Q L L M TCH200
 270 Q N S W Q T A D I S A R D S V G N T V L H A L V E V A D N T A D N T K F V T S M Y N E I L I L G hVR1
 283 E H - - E Q T D I T S R D S R G N N I L H A L V T V A E D F K T Q N D F V K R M Y D M I L L R S TCH200
 318 A K L H P T L K L E E L T N K K G M M P L A L A A G T G K I G V L A Y I L Q R E I Q E P E C R H hVR1
 329 G N W E - - - L E T T R N D G L T P L Q L A A K M G K A E I L K Y I L S R E I K E K R L R S TCH200
 366 L S R K F T E W A Y G P V H S S L Y D L S C I D T C E K N S V L E V I A Y S S S E T P N R H D M hVR1
 373 L S R K F T D W A Y G P V S S S L Y D L T N V D T T D N S V L E I T V Y N T N I D - N R H E M TCH200
 414 L L V E P L N R L L Q D K W D R F V K R I F Y F N F L V Y C L Y M I I F T M A A Y Y R P V D G L hVR1
 420 L T L E P L H T L L H M K W K K F A K H M F F L S F C F Y F F Y N I T L T L S Y Y R P R E E - TCH200
 462 P P F K M E K T G D Y F R V T G E I - - L S V L G G V Y F F F - - - - - R G I Q Y F L Q R hVR1
 467 - - - - - E A I P H P L A L T H K M G W L Q L L G R M F V L I W A M C I S V K E G I A I F L L R TCH200
 500 R P S M K T L F V D S Y S E M L F F L Q S L F M L A T V V L Y F S H L K E Y V A S M V F S L A L hVR1
 510 P S D L Q S I L S D A W F H F V F F I Q A V L V I L S V F L Y L F A Y K E Y L A C L V L A M A L TCH200
 548 G W T N M L Y Y T R G F Q Q M G I Y A V M I E K M I L R D L C R F M F V Y I V F L F G F S T A V hVR1
 558 G W A N M L Y Y T R G F Q S M G M Y S V M I Q K V I L H D V L K F L F V Y I V F L L G F G V A L TCH200
 596 V T L I E D G K N D S L P S E S T S H R W R G P A C R P P D S S Y N S L Y S T C L E L F K F T I hVR1
 606 A S L I E K C P K D N - - - - - K D C - - - - - S S Y G S F S D A V L E L F K L T I TCH200
 644 G M G D L E P T E N Y D F K A V F I I L L L A Y V I L T Y I L L N M L I A L M G E T V N K I A hVR1
 638 G L G D L N I Q Q N S K Y P I L F L P L L I T Y V I L T F V L L N M L I A L M G E T V E N V S TCH200
 692 Q E S K N I W K L Q R A I T I L D T E K S F L K C M R K A F R S G K L L Q V G Y T P D G K D D Y hVR1
 686 K E S E R I W R L Q R A R T I L E F E K M L P E W L R S R F R M G E L C K V A - - - - - E D D F TCH200
 740 R W C F R V D E V N W T T W N T N V G I I N E D P G N C E G V K R T L S F S L R S S R V S G R H hVR1
 729 R L C L R I N E V K W T E W K T H V S F L N E D P G P - - - - - V R R T A D F N - - - - - TCH200
 788 W K N F A L V P L L R E A S A R D R Q S A Q P E E V Y L R Q F S G S L K P E D A E V F K S P A A hVR1
 764 - - - - - K I Q D S S R N N S K T T - - - - - L N A F - - - - - E E V E E F - - - - - P E TCH200
 836 S G E K hVR1
 789 T S V . TCH200

FIG. 14

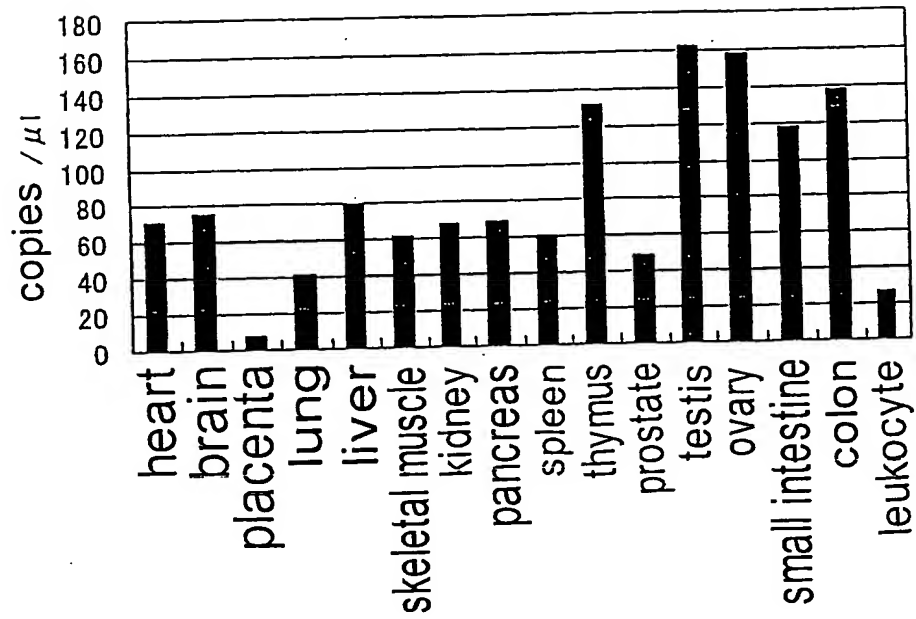


FIG. 15

1 M R A N C S S S S A C P A N S S E E E L P V G L E V H G N L E L V F T V V S T V hTCH230
 1 M S T D C A G N S T C P V N S T E E D P P V G M E G H A N L K L L F T V L S A V mTCH230
 41 M M G L L M F S L G C S V E I R K L W S H I R R P W G I A V G L L C Q F G L M P hTCH230
 41 M V G L V M F S F G C S V E S Q K L W L H L R R P W G I A V G L L S Q F G L M P mTCH230
 81 F T A Y L L A I S F S L K P V Q A I A V L I M G C C P G G T I S N I F T F W V D hTCH230
 81 L T A Y L L A I G F G L K P F Q A I A V L M M G S C P G G T I S N V L T F W V D mTCH230
 121 G D M D L S I S M T T C S T V A A L G M M P L C I Y L Y T W S W S L Q Q N L T I hTCH230
 121 G D M D L S I S M T T C S T V A A L G M M P L C L Y I Y T R S W T L T Q N L V I mTCH230
 161 P Y Q N I G I T L V C L T I P V A F G V Y V N Y R W P K Q S K I I L K I G A V V hTCH230
 161 P Y Q S I G I T L V S L V V P V A S G V Y V N Y R W P K Q A T V I L K V G A I L mTCH230
 201 G G V L L L V V A V A G V V L A K G S W N S D I T L L T I S F I F P L I G H V T hTCH230
 201 G G M L L L V V A V T G M V L A K G - W N T D V T L L V I S C I F P L V G H V T mTCH230
 241 G F L L A L F T H Q S W Q R C R T I S L E T G A Q N I Q M C I T M L Q L S F T A hTCH230
 240 G F L L A F L T H Q S W Q R C R T I S I E T G A Q N I Q L C I A M L Q L S F S A mTCH230
 281 E H L V Q M L S F P L A Y G L F Q L I D G F L I V A A Y Q T Y K R R L K N K H G hTCH230
 280 E Y L V Q L L N F A L A Y G L F Q V L H G L L I V A A Y Q A Y K R R Q K S K C R mTCH230
 321 K K N S G C T E V C H T R K S T S S R E T N A F L E V N E E G A I T P G P P G P hTCH230
 320 R Q H P D C P D V C Y E K Q P - - - R E T S A F L D K G D E A A V T L G P V Q P mTCH230
 361 M D C H R A L E P V G H I T S C E hTCH230
 357 E Q H H R A A E L T S H I P S C E mTCH230

FIG. 16

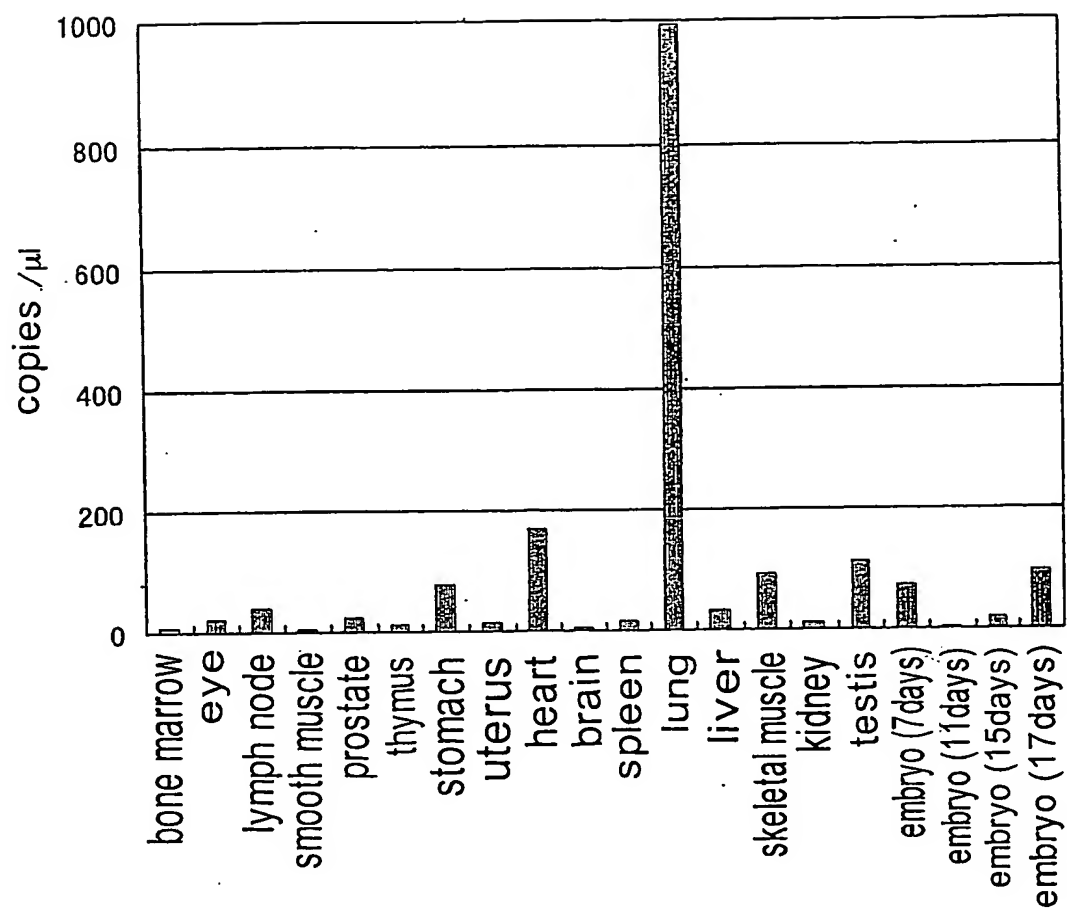


FIG. 17

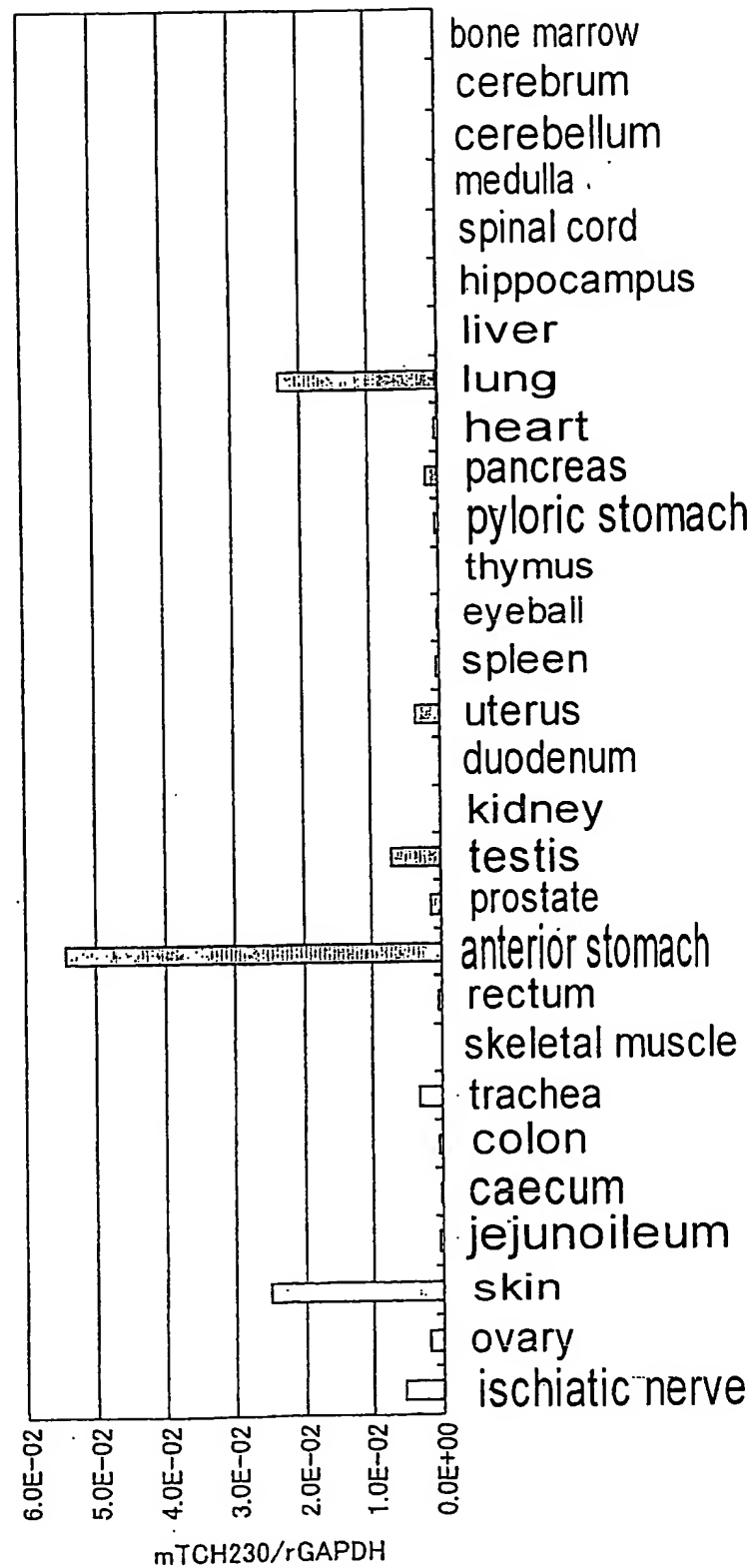


FIG. 18

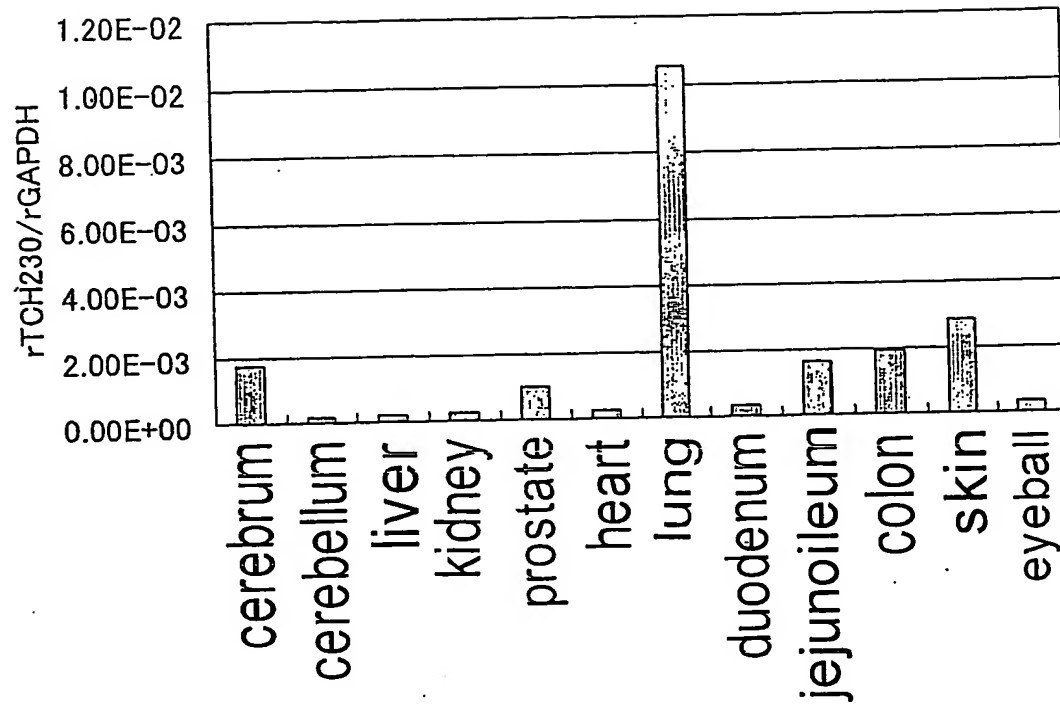


FIG. 19

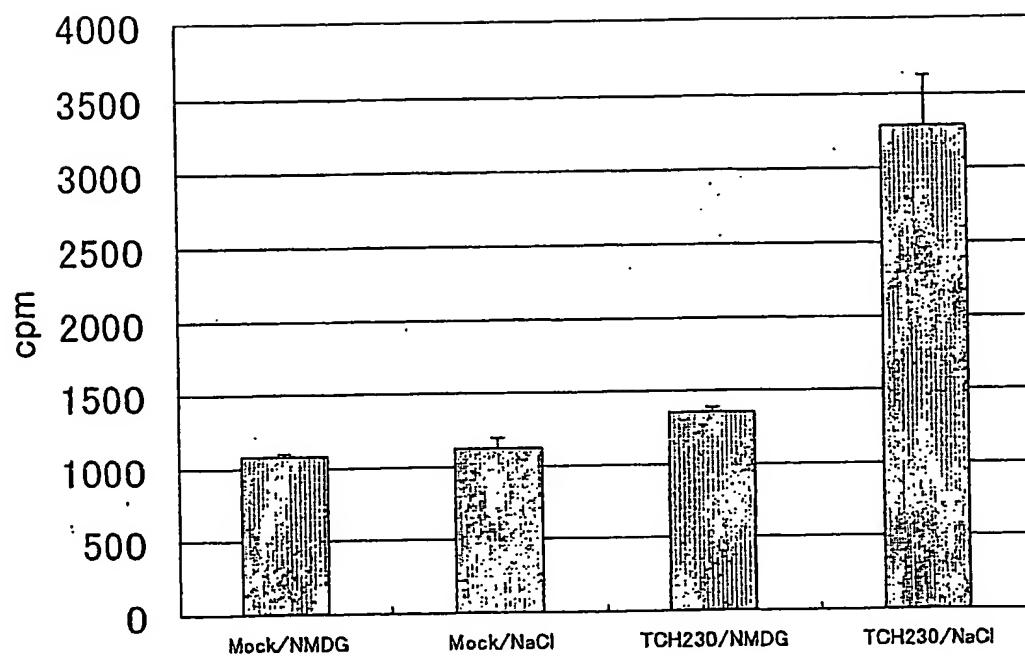


FIG. 20

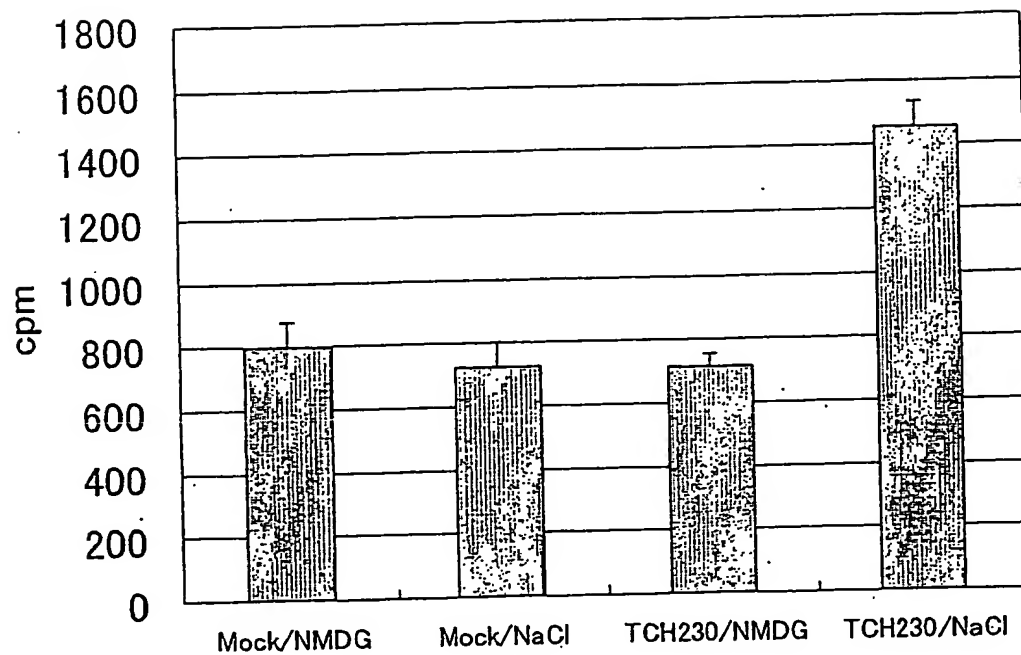


FIG. 21

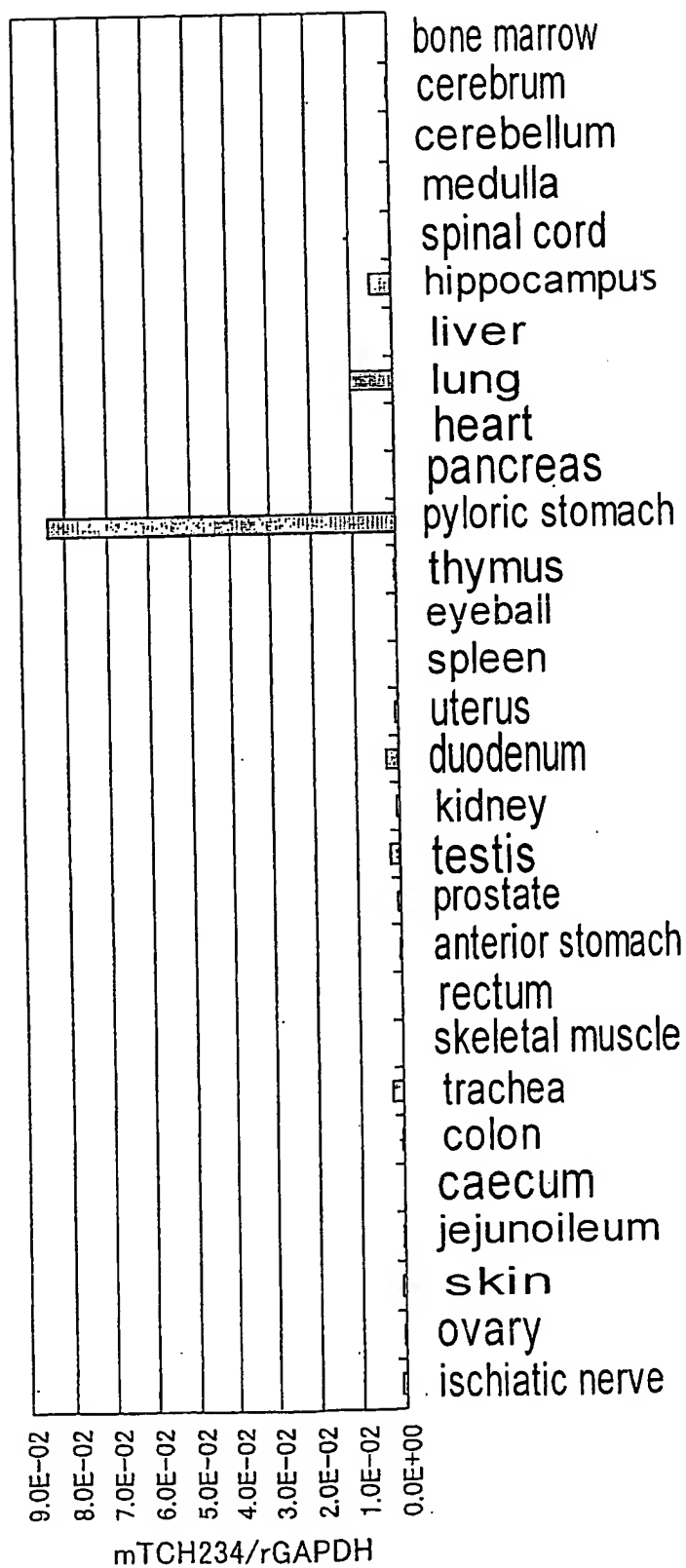


FIG. 22

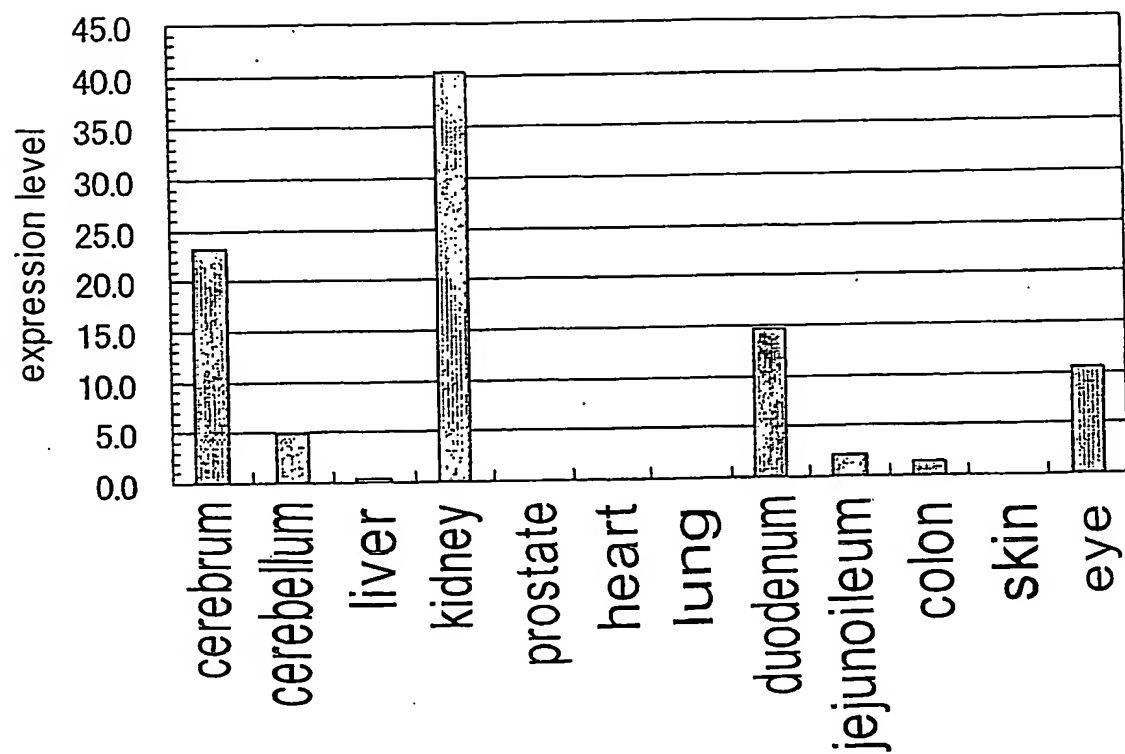


FIG. 23

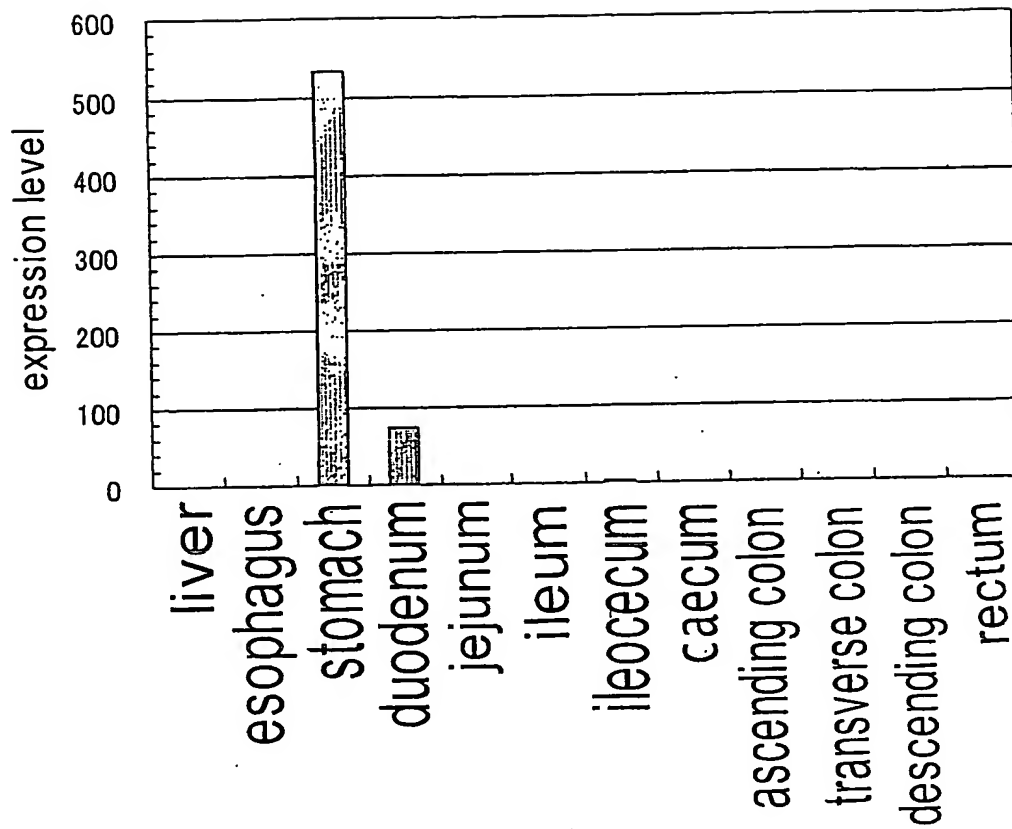


FIG. 24

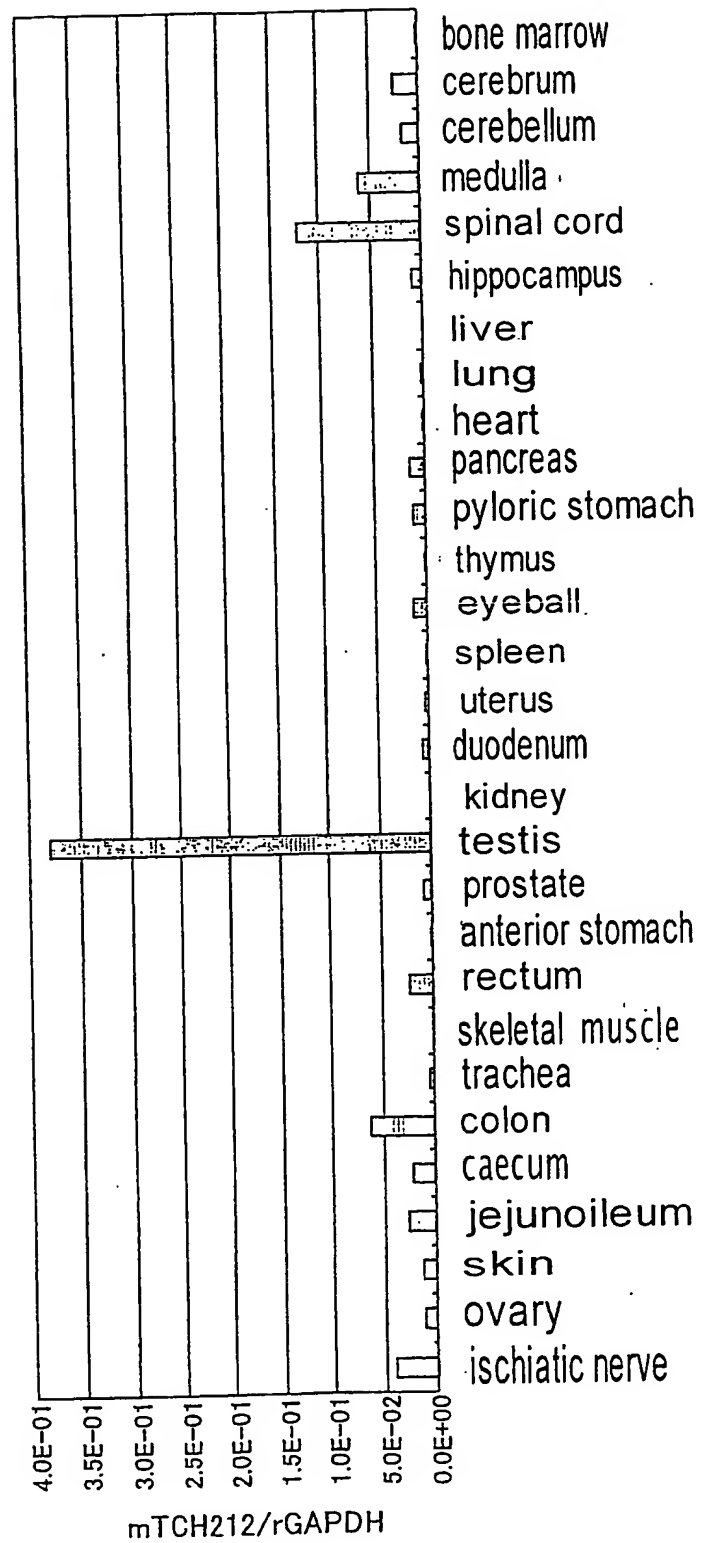


FIG. 25

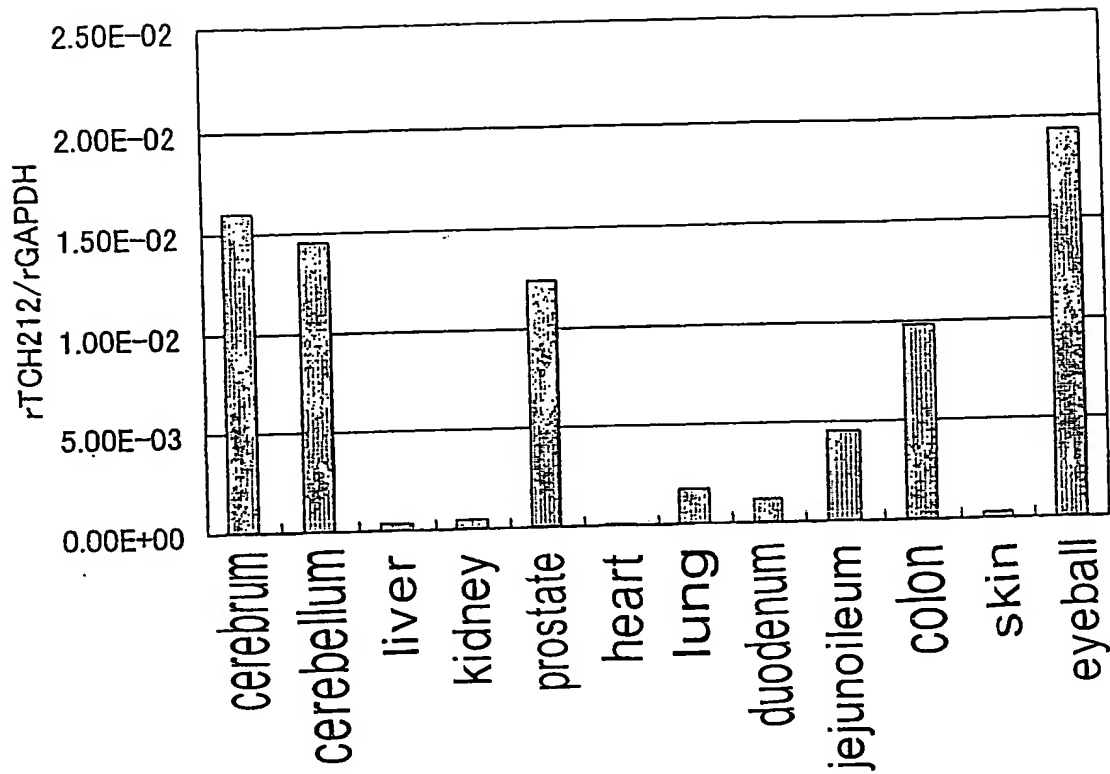


FIG. 26

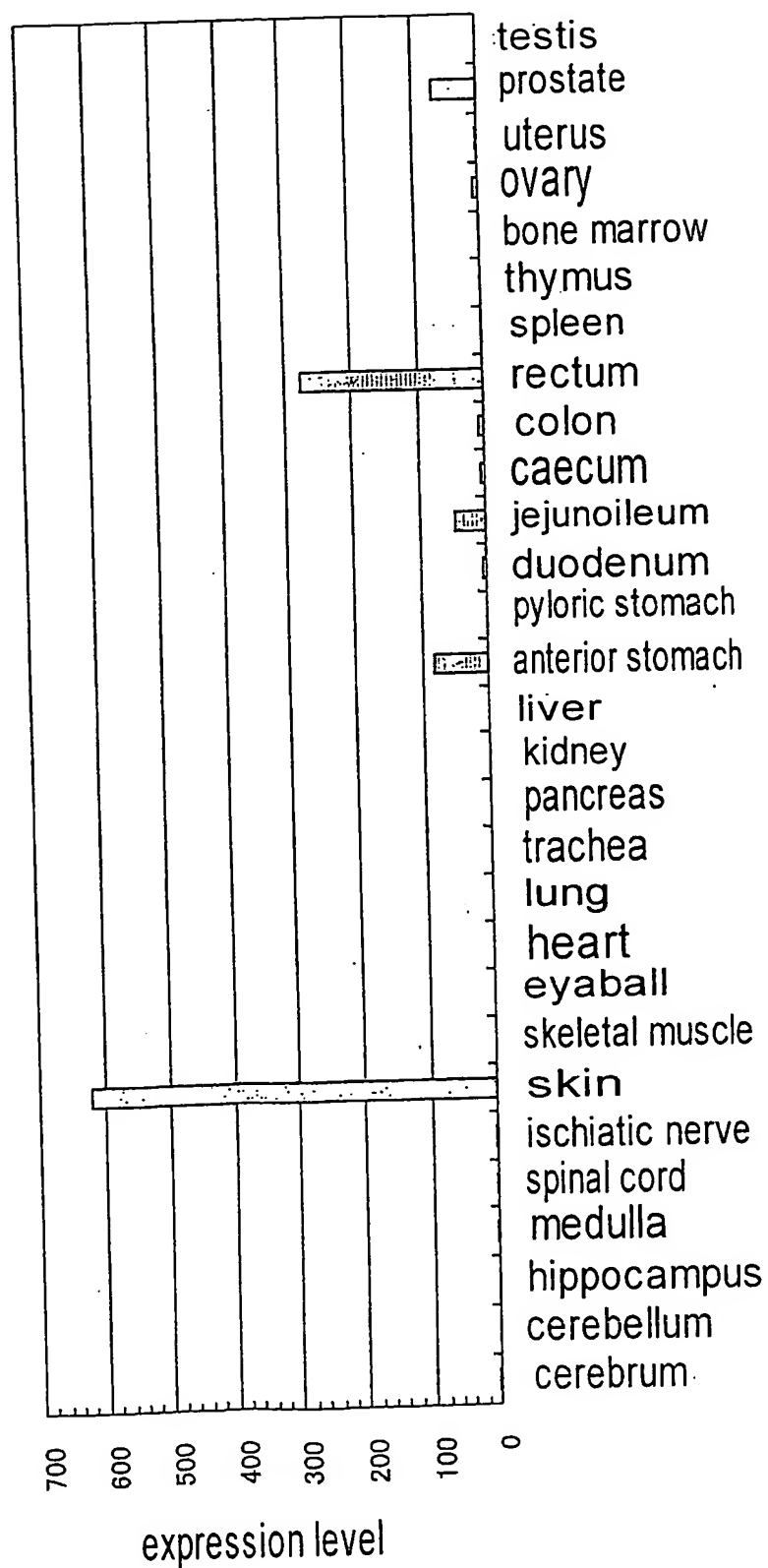


FIG. 27

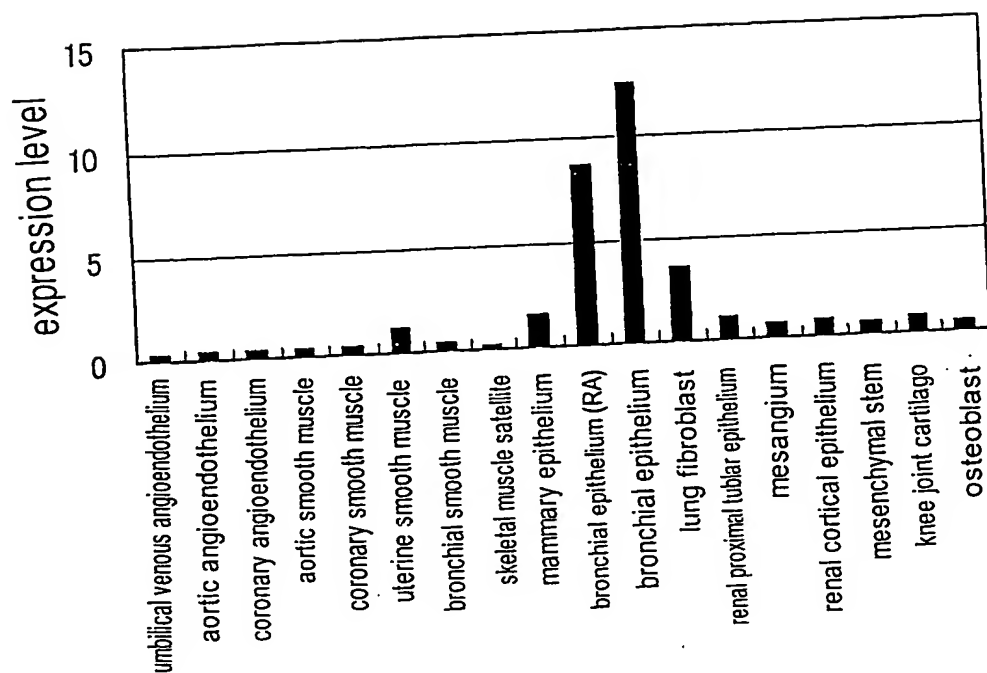


FIG. 28

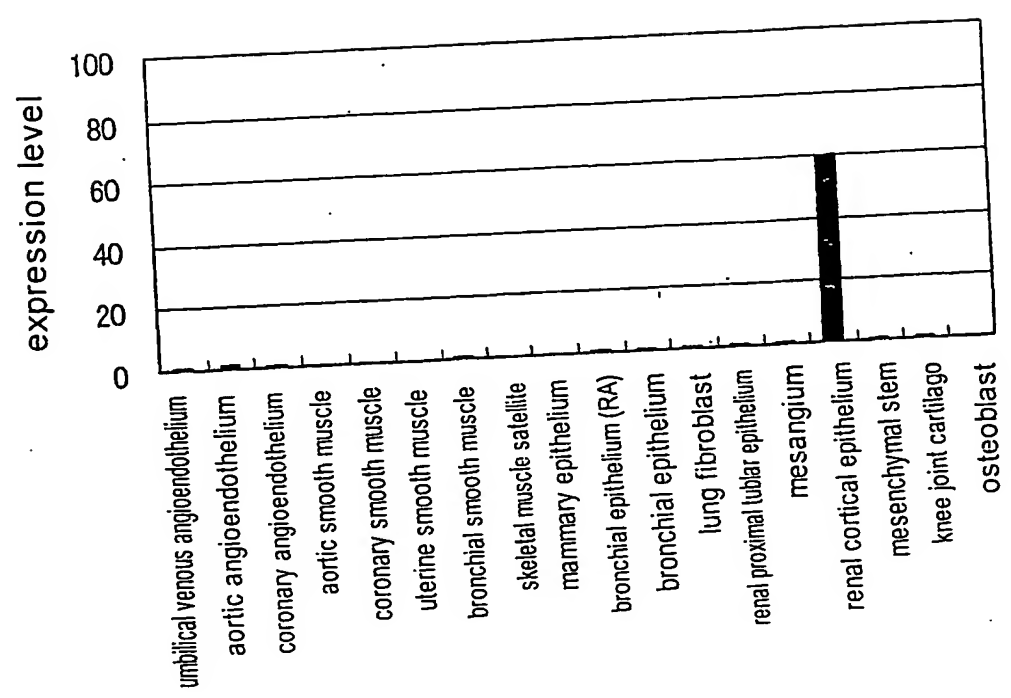


FIG. 29

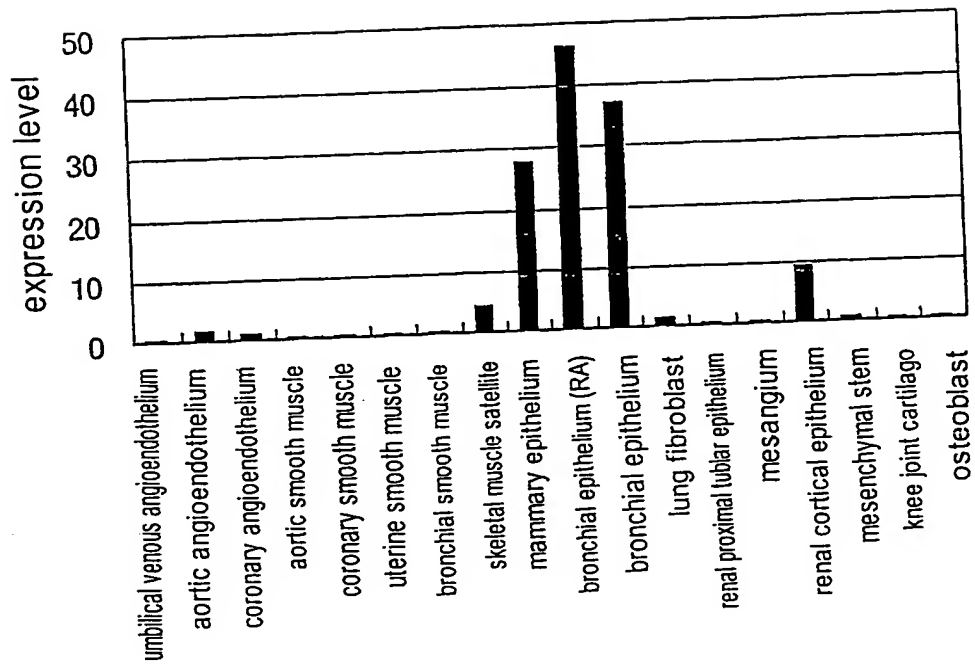


FIG. 30

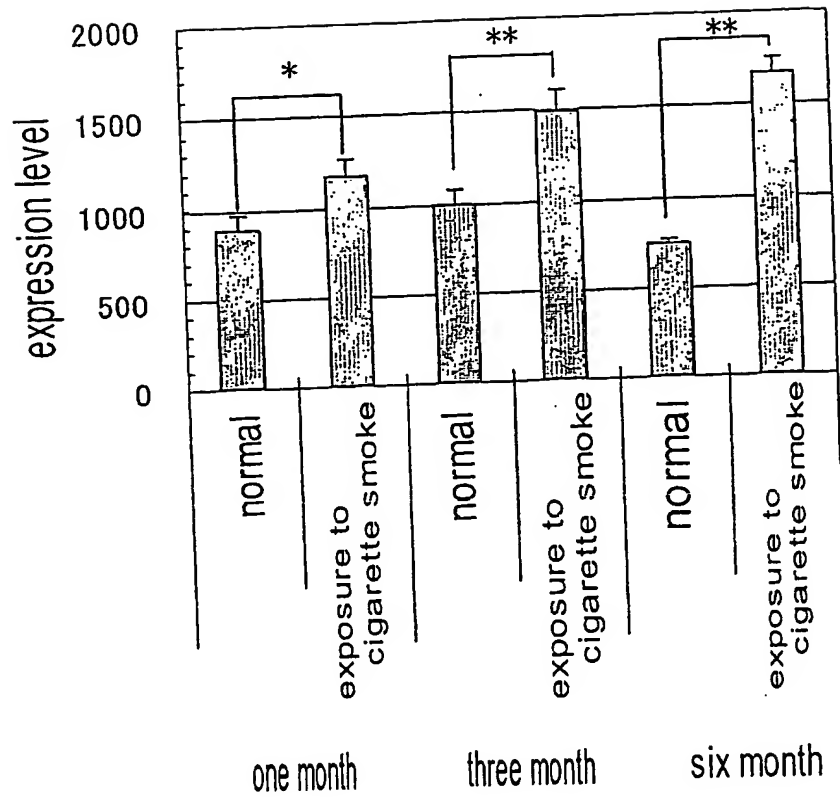


FIG. 31

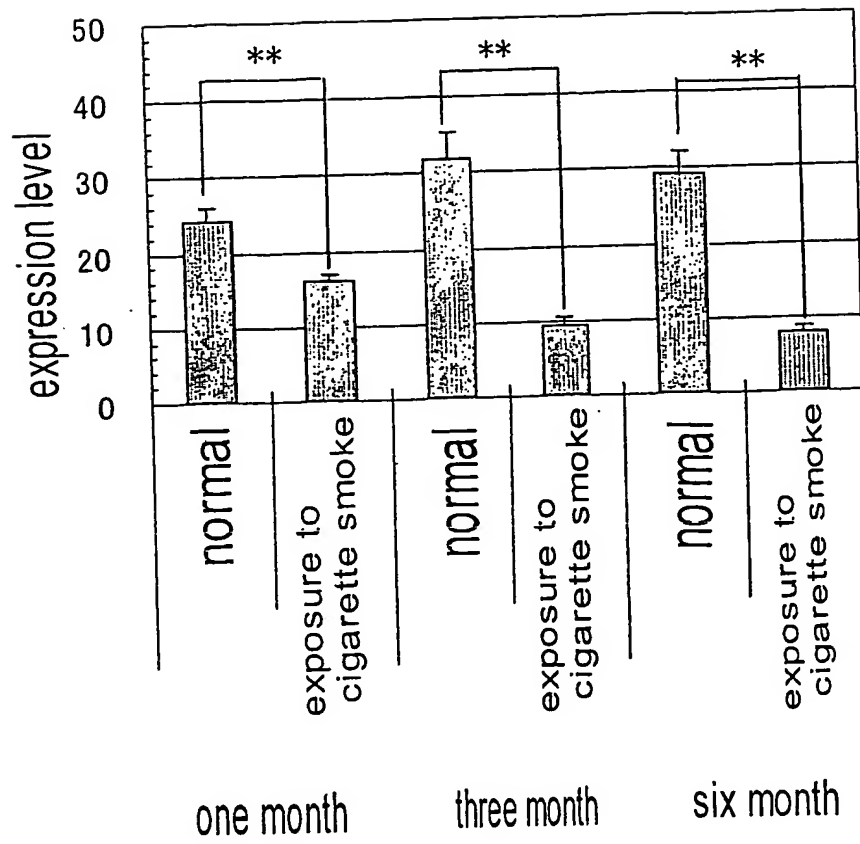


FIG. 32

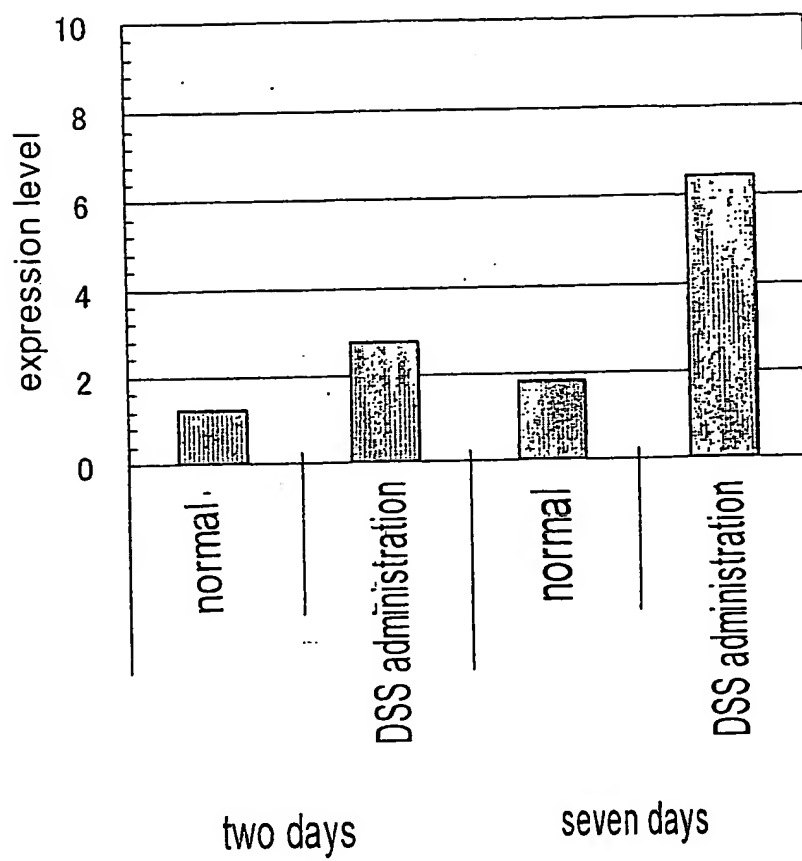


FIG. 33

